

RAW SEQUENCE LISTING **ERROR REPORT**

02D0
BIOTECHNOLOGY
SYSTEMS
BRANCH
#3

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number:

09/545,283

Art Unit / Team No. :

OLPE

Date Processed by STIC:

4/30/2000

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/545,283

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☒ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ☐ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ☐ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/545,283

DATE: 05/02/2000
 TIME: 08:51:02

Input Set : A:\C-type1.app
 Output Set: N:\CRF3\050200\I545283.raw

Does Not Comply
 Corrected Diskette Needed

3 <110> APPLICANT: Boyle, Bryan J.
 4 Ford, John E.
 5 Mize, Nancy K.
 6 Tang, Y. Tom
 7 Tillinghast, John
 8 Sinku, Ankura
 9 Liu, Chenghua
 10 Drmanac, Radoje T
 11 Dickson, Mark C
 12 Arterburn, Matthew C
 14 <120> TITLE OF INVENTION: Methods and Materials Relating to Novel C-Type Lectin
 15 Receptor-Like Polypeptides and Polynucleotides
 17 <130> FILE REFERENCE: HYS-5
 19 <140> CURRENT APPLICATION NUMBER: US/09/545,283
 20 <141> CURRENT FILING DATE: 2000-04-07
 22 <150> PRIOR APPLICATION NUMBER: 09/496,914
 23 <151> PRIOR FILING DATE: 2000-02-03
 25 <160> NUMBER OF SEQ ID NOS: 7
 27 <170> SOFTWARE: PatentIn Ver. 2.1
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 415
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Homo sapiens
 34 <400> SEQUENCE: 1
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 36 ccaggtgaag gtctggtcca tggcagtcgt atccatcttg ctccctcagtg tctgtttcac 120
 37 tgtgagttct gtggtgcctc acaattttat gtatagcaaa actgtcaaga ggctgtccaa 180
 38 gttacgagag tatcaacagt atcattcaag cctgacctgc gtcattggaag gaaaggacat 240
 39 agaagattgg agctgctgcc caacccttg gacttcattt cagtctagtt gctactttat 300
 40 ttctactggg atgcaatctt ggactaagag tcaaaagaac tgttctgtga tgggggctga 360
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 45 <211> LENGTH: 826
 46 <212> TYPE: DNA
 47 <213> ORGANISM: Homo sapiens
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 51 ccaggtgaag gtctggtcca tggcagtcgt atccatcttg ctccctcagtg tctgtttcac 120
 52 tgtgagttct gtggtgcctc acaattttat gtatagcaaa actgtcaaga ggctgtccaa 180
 53 gttacgagag tatcaacagt atcattcaag cctgacctgc gtcattggaag gaaaggacat 240
 54 agaagattgg agctgctgcc caacccttg gacttcattt cagtctagtt gctactttat 300
 55 ttctactggg atgcaatctt ggactaagag tcaaaagaac tgttctgtga tgggggctga 360
 56 tctggtgggt atcaacacca ggaagaaca ggatttcattc attcagaatc tgaaaagaaa 420
 57 ttcttcttat tttctggggc tgtcagatcc agggggctcg cgacattggc aatgggttga 480
 58 ccagacacca tacaatgaaa atgtcacgtg agtatagaat gagattcttg cactcagggtg 540
 59 aacccaataa ccttgatgag cgttggtcga taataaattt ccgttcttca gaagaatggg 600
 60 gctggaatga cattcactgt catgtacctc agaagtcaat ttgcaagatg aagaagatct 660

see item 10 on Eva Summary Sheet

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Input Set : A:\C-type1.app

Output Set: N:\CRF3\050200\I545283.raw

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61 acatataaat gaaatattct ccctggaaat gtgtttgggt tggcatccac cgttgtagaa 720
62 agctaaattg attttttaatt ttatgtgtaa gttttgtaca aggaatgccc ctaaaatgtt 780
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68 <212> TYPE: DNA
69 <213> ORGANISM: Homo sapiens
71 <220> FEATURE:
72 <221> NAME/KEY: CDS
73 <222> LOCATION: (43)..(747)
75 <400> SEQUENCE: 3
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77 Met Val Pro Glu
78 1
80 gaa gag cct caa gac cga gag aaa gga ctc tgg tgg ttc cag ttg aag 102
81 Glu Glu Pro Gln Asp Arg Glu Lys Gly Leu Trp Trp Phe Gln Leu Lys
82 5 10 15 20
84 gtc tgg tcc atg gca gtc gta tcc atc ttg ctc ctc agt gtc tgt ttc 150
85 Val Trp Ser Met Ala Val Val Ser Ile Leu Leu Ser Val Cys Phe
86 25 30 35
88 act gtg agt tct gtg cct cac aat ttt atg tat agc aaa act gtc 198
89 Thr Val Ser Ser Val Val Pro His Asn Phe Met Tyr Ser Lys Thr Val
90 40 45 50
92 aag agg ctg tcc aag tta cga gag tat caa cag tat cat tca agc ctg 246
93 Lys Arg Leu Ser Lys Leu Arg Glu Tyr Gln Gln Tyr His Ser Ser Leu
94 55 60 65
96 acc tgc gtc atg gaa gga aag gac ata gaa gat tgg agc tgc tgc cca 294
97 Thr Cys Val Met Glu Gly Lys Asp Ile Glu Asp Trp Ser Cys Cys Pro
98 70 75 80
100 acc cct tgg act tca ttt cag tct agt tgc tac ttt att tct act ggg 342
101 Thr Pro Trp Thr Ser Phe Gln Ser Ser Cys Tyr Phe Ile Ser Thr Gly
102 85 90 95 100
104 atg caa tct tgg act aag agt caa aag aac tgt tct gtg atg ggg gct 390
105 Met Gln Ser Trp Thr Lys Ser Gln Lys Asn Cys Ser Val Met Gly Ala
106 105 110 115
108 gat ctg gtg gtc atc aac acc acg gaa gaa cac gat ttc atc att cat 438
109 Asp Leu Val Val Ile Asn Thr Thr Glu Glu His Asp Phe Ile Ile His
110 120 125 130
112 aat ctg aaa aga aat tct tct tat ttt ctg ggg ctg tca cat cca cgg 486
113 Asn Leu Lys Arg Asn Ser Ser Tyr Phe Leu Gly Leu Ser His Pro Arg
114 135 140 145
116 ggt cgg cga cat tgg caa tgg gtt gac cac aca cca tac aat gaa aat 534
117 Gly Arg Arg His Trp Gln Trp Val Asp His Thr Pro Tyr Asn Glu Asn
118 150 155 160
120 gtc aca ttc tgg cac tca ggt gaa ccc aat aac ctt gat gag cgt tgt 582
121 Val Thr Phe Trp His Ser Gly Glu Pro Asn Asn Leu Asp Glu Arg Cys
122 165 170 175 180
124 gcg ata ata aat ttc cgc tct tca caa gaa tgg ggc tgg aat gac att 630
125 Ala Ile Ile Asn Phe Arg Ser Ser Gln Glu Trp Gly Trp Asn Asp Ile

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Input Set : A:\C-type1.app

Output Set: N:\CRF3\050200\I545283.raw

126 185 190 195
 128 cac tgt cat gta cct cac aag tca att tgc gag atg aag aag atc tac 678
 129 His Cys His Val Pro His Lys Ser Ile Cys Glu Met Lys Lys Ile Tyr
 130 200 205 210
 132 ata tac atg aaa tat tct ccc tgg aaa tgt gtt tgg gtt ggc atc cac 726
 133 Ile Tyr Met Lys Tyr Ser Pro Trp Lys Cys Val Trp Val Gly Ile His
 134 215 220 225
 136 cgc tgt aga aag cta aat tga ttttttaatt tatgtgtaag atttgtacaa 777
 137 Arg Cys Arg Lys Leu Asn
 138 230 235
 140 agaatgcccc taaatgtttc agcaggctgt cacctattac acttatgata taatccattc 837
 142 acacattcaa aaaaaaaaaa g 858
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 146 <211> LENGTH: 234
 147 <212> TYPE: PRT
 148 <213> ORGANISM: Homo sapiens
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 152 1 5 10 15
 153 Phe Gln Leu Lys Val Trp Ser Met Ala Val Val Ser Ile Leu Leu Leu
 154 20 25 30
 155 Ser Val Cys Phe Thr Val Ser Ser Val Val Pro His Asn Phe Met Tyr
 156 35 40 45
 157 Ser Lys Thr Val Lys Arg Leu Ser Lys Leu Arg Glu Tyr Gln Gln Tyr
 158 50 55 60
 159 His Ser Ser Leu Thr Cys Val Met Glu Gly Lys Asp Ile Glu Asp Trp
 160 65 70 75 80
 161 Ser Cys Cys Pro Thr Pro Trp Thr Ser Phe Gln Ser Ser Cys Tyr Phe
 162 85 90 95
 163 Ile Ser Thr Gly Met Gln Ser Trp Thr Lys Ser Gln Lys Asn Cys Ser
 164 100 105 110
 165 Val Met Gly Ala Asp Leu Val Val Ile Asn Thr Thr Glu Glu His Asp
 166 115 120 125
 167 Phe Ile Ile His Asn Leu Lys Arg Asn Ser Ser Tyr Phe Leu Gly Leu
 168 130 135 140
 169 Ser His Pro Arg Gly Arg Arg His Trp Gln Trp Val Asp His Thr Pro
 170 145 150 155 160
 171 Tyr Asn Glu Asn Val Thr Phe Trp His Ser Gly Glu Pro Asn Asn Leu
 172 165 170 175
 173 Asp Glu Arg Cys Ala Ile Ile Asn Phe Arg Ser Ser Gln Glu Trp Gly
 174 180 185 190
 175 Trp Asn Asp Ile His Cys His Val Pro His Lys Ser Ile Cys Glu Met
 176 195 200 205
 177 Lys Lys Ile Tyr Ile Tyr Met Lys Tyr Ser Pro Trp Lys Cys Val Trp
 178 210 215 220
 179 Val Gly Ile His Arg Cys Arg Lys Leu Asn
 180 225 230
 184 <210> SEQ ID NO: 5
 185 <211> LENGTH: 14

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/545,283

DATE: 05/02/2000
 TIME: 08:51:02

Input Set : A:\C-typel.app
 Output Set: N:\CRF3\050200\I545283.raw

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195 <211> LENGTH: 193
196 <212> TYPE: PRT
197 <213> ORGANISM: Homo sapiens
199 <400> SEQUENCE: 6
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201 1 5 10 15
203 Leu Arg Glu Tyr Gln Gln Tyr His Ser Ser Leu Thr Cys Val Met Glu
204 20 25 30
206 Gly Lys Asp Ile Glu Asp Trp Ser Cys Cys Pro Thr Pro Trp Thr Ser
207 35 40 45
209 Phe Gln Ser Ser Cys Tyr Phe Ile Ser Thr Gly Met Gln Ser Trp Thr
210 50 55 60
212 Lys Ser Gln Lys Asn Cys Ser Val Met Gly Ala Asp Leu Val Val Ile
213 65 70 75 80
215 Asn Thr Thr Glu Glu His Asp Phe Ile Ile His Asn Leu Lys Arg Asn
216 85 90 95
218 Ser Ser Tyr Phe Leu Gly Leu Ser His Pro Arg Gly Arg Arg His Trp
219 100 105 110
221 Gln Trp Val Asp His Thr Pro Tyr Asn Glu Asn Val Thr Phe Trp His
222 115 120 125
224 Ser Gly Glu Pro Asn Asn Leu Asp Glu Arg Cys Ala Ile Ile Asn Phe
225 130 135 140
227 Arg Ser Ser Gln Glu Trp Gly Trp Asn Asp Ile His Cys His Val Pro
228 145 150 155 160
230 His Lys Ser Ile Cys Glu Met Lys Lys Ile Tyr Ile Tyr Met Lys Tyr
231 165 170 175
233 Ser Pro Trp Lys Cys Val Trp Val Gly Ile His Arg Cys Arg Lys Leu
234 180 185 190
236 Asn
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242 <212> TYPE: PRT
243 <213> ORGANISM: Homo sapiens
245 <400> SEQUENCE: 7
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247 1 5 10 15
249 Asn Cys

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/545,283

DATE: 05/02/2000

TIME: 08:51:03

Input Set : A:\C-type1.app

Output Set: N:\CRF3\050200\I545283.raw

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L:41 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:41 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:41 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:41 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:138 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3